

STERN29.002APC SEQLIST.TXT

SEQUENCE LISTING

<110> Giannotta, Fabrizio
Filee, Patrice
Galleni, Moreno
Frere, Jean-Marie
Joris, Bernard
Brans, Alain
Ruth, Nadia

<120> HYBRID PROTEINS OF ACTIVE-SITE SERINE
BETA-LACTAMASE

<130> STERN29.002APC

<150> PCT/EP2005/050174

<151> 2005-01-17

<150> EP 04075430.1

<151> 2001-02-11

<160> 68

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 858

<212> DNA

<213> Escherichia coli

<400> 1

ccaatgctta	atcagtgagg	cacctatctc	agcgatctgt	ctatttcggt	catccatagt	60
tgcctgactc	cccgtcgtgt	agataactac	gatacgggag	ggcttaccat	ctggccccag	120
tgctgcaatg	ataccgcgag	acccacgctc	accggctcca	gatttatcag	caataaacca	180
gccagccgga	agggccgagc	gcagaagtgg	tcctgcaact	ttatccgcct	ccatccagtc	240
tattaattgt	tgccgggaag	ctagagtaag	tagttcgcca	gttaatagtt	tgcgcaacgt	300
tggttgccatt	gctgcaggca	tcgtgggtgc	acgctcgtcg	tttggtatgg	cttcattcag	360
ctccggttcc	caacgatcaa	ggcgagttac	atgatcccc	atggttgca	aaaaagcgg	420
tagctccttc	ggctctccga	tcgttggtcag	aagtaagttg	gccgcagttg	tatcactcat	480
ggttatggca	gcactgcata	attctcttac	tgctatgcc	tccgtaagat	gcttttctgt	540
gactgggtgag	tactcaacca	agtcattctg	agaatagtgt	atgcggcgac	cgagttgctc	600
ttgcccggcg	tcaacacggg	ataataccgc	gccacatagc	agaacttta	aagtgtcat	660
cattgaaaa	cgttcttcg	ggcgaaaact	ctcaaggatc	ttaccgctgt	tgagatccag	720
ttcgatgtaa	cccactcgtg	cacccaactg	atcttcagca	tcttttactt	tcaccagcgt	780
ttctgggtga	gcaaaaacag	gaaggcaaaa	tgccgcaaaa	aagggaataa	gggcgacacg	840
gaaatgttga	atactcat					858

<210> 2

<211> 921

<212> DNA

<213> Bacillus licheniformis

<400> 2

atgaaattat	ggttcagttac	tttaaaactg	aaaaaggctg	cagcagtggt	gcttttctct	60
tgcgtcgcgc	ttgcaggatg	cgctaacaat	caaacgaatg	cctcgcaacc	tgccgagaag	120
aatgaaaaga	cggagatgaa	agatgatttt	gcaaaaactg	aggaacaatt	tgatgcaaaa	180
ctcggtatct	ttgcattgga	tacaggtaca	aaccggacgg	tagcgtatcg	gccggatgag	240
ggttttgctt	ttgcttcgac	gattaaggct	ttactgtag	gcgtgctttt	gcaacagaaa	300
tcaatagaag	atctgaacca	gagaataaca	tatacacgtg	atgatcttgt	aaactacaac	360
ccgattacgg	aaaagcacgt	tgatacggga	atgacgtca	aagagcttgc	ggatgcttcg	420
cttcgatata	gtgacaatgc	ggcacagaat	ctcattctta	aacaaattgg	cggacctgaa	480
agtttgaaaa	aggaactgag	gaagattggt	gatgaggtta	caaattccga	acgattcgaa	540

STERN29.002APC SEQLIST.TXT

```

ccagagttaa atgaagtgaa tccgggtgaa actcaggata ccagtacagc aagagcactt 600
gtcacaagcc ttcgagcctt tgctcttgaa gataaacttc caagtgaata acgcgagctt 660
ttaatcgatt ggatgaaacg aaataccact ggagacgcct taatccgtgc cggtgtgccg 720
gacggttggg aagtggctga taaaactgga gcggcatcat atggaaccgc gaatgacatt 780
gccatcattt ggccgcaaaa aggagatcct gtcgttcttg cagtattatc cagcagggat 840
aaaaaggacg ccaagtatga tgataaactt attgcagagg caacaaaggt ggtaatgaaa 900
gccttaaca tgaacggcaa a

```

<210> 3

<211> 975

<212> DNA

<213> Streptomyces cacaoi

<400> 3

```

atgctgtatcc gtcccacccg tcgtcttctc ctggcgcgcg tcgcgccgct cgccctcggt 60
ccgctggttg cctgcggtca ggcgtcgggc tccgagagcg gccagcagcc cggcctcggc 120
ggttgcggga cgagcgcaca cggctcggcg gacgcccacg agaaggagtt ccggcgctg 180
gagaagaagt tcgacgcccc ccctggcgctc tacgccatcg acaccgcga cggccaggag 240
atcaccaccc gggccgacga gcgcttcgcc tacggctcga cttcaaggc cctccaggcg 300
ggcgcgatcc ttgcgcaagt tctccgagac gggcgcgaaag tccggcgggg cgccgaggcc 360
gacggcatgg acaagggtgt ccactacggg caggacgcga tcctgccccaa ctcaccggtg 420
accgagaagc acgtcgcgga cggcatgtcc ctgctcgagc tgtgctgacg cgctcggtgg 480
tacagcgaca acaccgcggc caacctgtct ttcgaccagc tcggcgggcg aaggggtca 540
acgcgggtcc tcaagcagct cggcgaccac accacgagca tggaccgcta cgagcaggag 600
ctgggctcgg ccgtccccgg cgacccccgg gacaccagca cgccgcgcgc gttcgccgag 660
gacctgcgcg ccttcgccgt cgaggacggc gagaaggccg ccctcgcgcc caacgaccgc 720
gagcagctga acgactggat gagcgggagc aggaccggcg acgcgtgat ccgggcccgt 780
gtgccgaagg actggaaggt ggaggacaag agcggccagg tcaagtacgg caccgggaac 840
gacatcgccg tcgtccgccc gcccgggccg gcgcccgcgc tcgtctcggt gatgagccac 900
ggcgacaccc aggacgcca gccgcacgac gagctggtgg ccgaggcccg cctcgtcgtc 960
gccgacggtc tgaag

```

<210> 4

<211> 286

<212> PRT

<213> Escherichia coli

<400> 4

```

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
1      5      10      15
Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
20      25      30
Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
35      40      45
Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
50      55      60
Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
65      70      75      80
Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
85      90      95
Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
100     105     110
Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
115     120     125
Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
130     135     140
Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
145     150     155     160
Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
165     170     175
Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
180     185     190
Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp

```

STERN29.002APC SEQLIST.TXT

Met	Glu	195	Ala	Asp	Lys	Val	Ala	200	Gly	Pro	Leu	Leu	Arg	205	Ser	Ala	Leu	Pro
	210						215						220					
Ala	Gly	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser			
225					230					235					240			
Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile			
				245					250					255				
Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn			
			260					265					270					
Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp					
		275					280					285						

<210> 5
 <211> 307
 <212> PRT
 <213> Bacillus licheniformis

<400> 5

Met	Lys	Leu	Trp	Phe	Ser	Thr	Leu	Lys	Leu	Lys	Lys	Ala	Ala	Ala	Val
1				5				10						15	
Leu	Leu	Phe	Ser	Cys	Val	Ala	Leu	Ala	Gly	Cys	Ala	Asn	Asn	Gln	Thr
			20					25				30			
Asn	Ala	Ser	Gln	Pro	Ala	Glu	Lys	Asn	Glu	Lys	Thr	Glu	Met	Lys	Asp
		35					40					45			
Asp	Phe	Ala	Lys	Leu	Glu	Glu	Gln	Phe	Asp	Ala	Lys	Leu	Gly	Ile	Phe
	50					55				60					
Ala	Leu	Asp	Thr	Gly	Thr	Asn	Arg	Thr	Val	Ala	Tyr	Arg	Pro	Asp	Glu
65					70					75				80	
Arg	Phe	Ala	Phe	Ala	Ser	Thr	Ile	Lys	Ala	Leu	Thr	Val	Gly	Val	Leu
				85					90					95	
Leu	Gln	Gln	Lys	Ser	Ile	Glu	Asp	Leu	Asn	Gln	Arg	Ile	Thr	Tyr	Thr
			100					105					110		
Arg	Asp	Asp	Leu	Val	Asn	Tyr	Asn	Pro	Ile	Thr	Glu	Lys	His	Val	Asp
		115					120					125			
Thr	Gly	Met	Thr	Leu	Lys	Glu	Leu	Ala	Asp	Ala	Ser	Leu	Arg	Tyr	Ser
	130					135				140					
Asp	Asn	Ala	Ala	Gln	Asn	Leu	Ile	Leu	Lys	Gln	Ile	Gly	Gly	Pro	Glu
145					150					155				160	
Ser	Leu	Lys	Lys	Glu	Leu	Arg	Lys	Ile	Gly	Asp	Glu	Val	Thr	Asn	Pro
				165					170					175	
Glu	Arg	Phe	Glu	Pro	Glu	Leu	Asn	Glu	Val	Asn	Pro	Gly	Glu	Thr	Gln
			180					185					190		
Asp	Thr	Ser	Thr	Ala	Arg	Ala	Leu	Val	Thr	Ser	Leu	Arg	Ala	Phe	Ala
		195					200					205			
Leu	Glu	Asp	Lys	Leu	Pro	Ser	Glu	Lys	Arg	Glu	Leu	Leu	Ile	Asp	Trp
	210					215						220			
Met	Lys	Arg	Asn	Thr	Thr	Gly	Asp	Ala	Leu	Ile	Arg	Ala	Gly	Val	Pro
225					230					235					240
Asp	Gly	Trp	Glu	Val	Ala	Asp	Lys	Thr	Gly	Ala	Ala	Ser	Tyr	Gly	Thr
				245					250					255	
Arg	Asn	Asp	Ile	Ala	Ile	Ile	Trp	Pro	Pro	Lys	Gly	Asp	Pro	Val	Val
			260					265					270		
Leu	Ala	Val	Leu	Ser	Ser	Arg	Asp	Lys	Lys	Asp	Ala	Lys	Tyr	Asp	Asp
		275					280					285			
Lys	Leu	Ile	Ala	Glu	Ala	Thr	Lys	Val	Val	Met	Lys	Ala	Leu	Asn	Met
	290					295					300				
Asn	Gly	Lys													
305															

<210> 6
 <211> 325

STERN29.002APC SEQLIST.TXT

<212> PRT

<213> Streptomyces cacaoi

<400> 6

```

Met Arg Ile Arg Pro Thr Arg Arg Leu Leu Leu Gly Ala Val Ala Pro
 1      5      10      15
Leu Ala Leu Val Pro Leu Val Ala Cys Gly Gln Ala Ser Gly Ser Glu
 20      25      30
Ser Gly Gln Gln Pro Gly Leu Gly Gly Cys Gly Thr Ser Ala His Gly
 35      40      45
Ser Ala Asp Ala His Glu Lys Glu Phe Arg Ala Leu Glu Lys Lys Phe
 50      55      60
Asp Ala His Pro Gly Val Tyr Ala Ile Asp Thr Arg Asp Gly Gln Glu
 65      70      75      80
Ile Thr His Arg Ala Asp Glu Arg Phe Ala Tyr Gly Ser Thr Phe Lys
 85      90      95
Ala Leu Gln Ala Gly Ala Ile Leu Ala Gln Val Leu Arg Asp Gly Arg
 100      105      110
Glu Val Arg Gly Ala Glu Ala Asp Gly Met Asp Lys Val Val His
 115      120      125
Tyr Gly Gln Asp Ala Ile Leu Pro Asn Ser Pro Val Thr Glu Lys His
 130      135      140
Val Ala Asp Gly Met Ser Leu Arg Glu Leu Cys Asp Ala Val Val Ala
 145      150      155      160
Tyr Ser Asp Asn Thr Ala Ala Asn Leu Leu Phe Asp Gln Leu Gly Gly
 165      170      175
Arg Arg Gly Ser Thr Arg Val Leu Lys Gln Leu Gly Asp His Thr Thr
 180      185      190
Ser Met Asp Arg Tyr Glu Gln Glu Leu Gly Ser Ala Val Pro Gly Asp
 195      200      205
Pro Arg Asp Thr Ser Thr Pro Arg Ala Phe Ala Glu Asp Leu Arg Ala
 210      215      220
Phe Ala Val Glu Asp Gly Glu Lys Ala Ala Leu Ala Pro Asn Asp Arg
 225      230      235      240
Glu Gln Leu Asn Asp Trp Met Ser Gly Ser Arg Thr Gly Asp Ala Leu
 245      250      255
Ile Arg Ala Gly Val Pro Lys Asp Trp Lys Val Glu Asp Lys Ser Gly
 260      265      270
Gln Val Lys Tyr Gly Thr Arg Asn Asp Ile Ala Val Val Arg Pro Pro
 275      280      285
Gly Arg Ala Pro Ile Val Val Ser Val Met Ser His Gly Asp Thr Gln
 290      295      300
Asp Ala Glu Pro His Asp Glu Leu Val Ala Glu Ala Gly Leu Val Val
 305      310      315      320
Ala Asp Gly Leu Lys
 325

```

<210> 7

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer

<400> 7

tcagttaaca atttcaacaa agaacaacaa aatgct

36

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

STERN29.002APC SEQLIST.TXT

<220>
 <223> synthetic primer

<400> 8
 tcgaaatttt ttgttgcttt cctcttttgg 30

<210> 9
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic primer

<400> 9
 catatgaaaa agaaaaacat ttattcaatt cgt 33

<210> 10
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic primer

<400> 10
 ggatccttat agttcgcgac gacgtccagc taa 33

<210> 11
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic primer

<400> 11
 cgaggactca ggctcaccca gaaacgctgg tg 32

<210> 12
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic primer

<400> 12
 cggaattct caccaatgct taatcagtga ggcacc 36

<210> 13
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic primer

<400> 13
 ggctgtactt acaaattaat ccttaatggt aaaacattg 39

<210> 14

STERN29.002APC SEQLIST.TXT

<211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic primer

 <400> 14
 ctctctttca gttaccgtaa aggtcttagt cgc 33

 <210> 15
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic primer

 <400> 15
 aggttttatc catacgacgt cccggactac gccacaact 39

 <210> 16
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic primer

 <400> 16
 agttgtggcg tagtccggga cgtcgtatgg ataaaacct 39

 <210> 17
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic primer

 <400> 17
 ctcgagaaaa gaaatttggt gaatttcac 30

 <210> 18
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic primer

 <400> 18
 gcaacgtgga gtgctccctc tgcagtgttt 30

 <210> 19
 <211> 90
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic primer

 <400> 19

STERN29.002APC SEQLIST.TXT

ccgatcatca aactttctcaa gctgcttaaa ctctctgcgc ggaaacttct caagctgctt 60
aaactctgc cggatcagga gtttaagcag 90

<210> 20
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 20
ctgcttaaac tcctgatccg gcaggagttt aagcagcttg agaagtttcc ggcgcaggag 60
tttaagcagc ttgagaagtt tgatgatcgg 90

<210> 21
<211> 54
<212> DNA
<213> Escherichia coli

<400> 21
aacacgtttt actgctgcga actttgctgc aaccagcat gcgcagggtg ctac 54

<210> 22
<211> 18
<212> PRT
<213> Escherichia coli

<400> 22
Asn Thr Phe Tyr Cys Cys Glu Leu Cys Cys Asn Pro Ala Cys Ala Gly
1 5 10 15
Cys Tyr

<210> 23
<211> 201
<212> DNA
<213> Staphylococcus aureus

<400> 23
tcagtgaaca atttcaaca agaacaaca aatgctttct atgaaatttt acatttacct 60
aacttaactg aagaacaacg taacggcttc atccaaagcc tttaaagacga tccttcagtg 120
agcaaagaaa ttttagcaga agctaaaaag ctaaacgatg ctcaagcacc aaaagaggaa 180
gacaacaaga aaaaatttcg a 201

<210> 24
<211> 67
<212> PRT
<213> Staphylococcus aureus

<400> 24
Ser Val Asn Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15
Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln
20 25 30
Ser Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala
35 40 45
Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Lys Lys
50 55 60
Lys Phe Arg
65

STERN29.002APC SEQLIST.TXT

<210> 25
 <211> 375
 <212> DNA
 <213> Staphylococcus aureus

<400> 25
 tcagtgaaca atttcaacaa agaacaacaa aatgctttct atgaaatctt gaacatgcct 60
 aacttgaacg aagaacaacg caatggtttc atccaaagct taaaagatga cccaagtcaa 120
 agtgctaacc ttttagcaga agctaaaaag ttaaatgaat ctcaagcacc gaaagctgat 180
 aacaatttca acaaagaaca acaaaatgct ttctatgaaa ttttacattt acctaactta 240
 actgaagaac aacgtaacgg cttcatccaa agccttaaag acgatccttc agtgagcaaa 300
 gaaatttttag cagaagctaa aaagctaaac gatgctcaag caccaaaaga ggaagacaac 360
 aagaaaaaat ttcga 375

<210> 26
 <211> 125
 <212> PRT
 <213> Staphylococcus aureus

<400> 26
 Ser Val Asn Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
 1 5 10 15
 Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln
 20 25 30
 Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala
 35 40 45
 Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn
 50 55 60
 Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
 65 70 75 80
 Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro
 85 90 95
 Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
 100 105 110
 Gln Ala Pro Lys Glu Glu Asp Asn Lys Lys Lys Phe Arg
 115 120 125

<210> 27
 <211> 177
 <212> DNA
 <213> Streptococcus pyogenes

<400> 27
 ggctgtactt acaaattaat ccttaatggt aaaacattga aaggccaaac aactactgaa 60
 gctgttgatg ctgctactgc agaaaaagtc ttcaaacaat acgctaacga caacggtggt 120
 gacggtgaat ggacttacga cgatgcgact aagaccttta cggtactga aagagaa 177

<210> 28
 <211> 59
 <212> PRT
 <213> Streptococcus pyogenes

<400> 28
 Gly Cys Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys Gly Gln
 1 5 10 15
 Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys
 20 25 30
 Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp
 35 40 45
 Ala Thr Lys Thr Phe Thr Val Thr Glu Arg Glu
 50 55

STERN29.002APC SEQLIST.TXT

<210> 29
 <211> 387
 <212> DNA
 <213> Streptococcus pyogenes

<400> 29
 ggctgtactt acaaattaat ccttaatggt aaaacattga aaggccaaac aactactgaa 60
 gctgttgatg ctgctactgc agaaaaagtc ttcaaacaat acgctaacga caacgggtgtt 120
 gacgggtgaat ggacttacga cgatgcgact aagaccttta cagttactga aaaaccagaa 180
 gtgatcgatg cgtctgaatt aacaccagcc gtgacaactt acaaacttgt tattaatggt 240
 aaaacattga aaggcgaaac aactactaaa gcagtagacg cagaaactgc agaaaaagcc 300
 ttcaaacaat acgctaacga caacgggtgtt gatgggtgtt ggacttatga tgatgcgact 360
 aagaccttta cggttaactga aagagag 387

<210> 30
 <211> 129
 <212> PRT
 <213> Streptococcus pyogenes

<400> 30
 Gly Cys Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys Gly Gln
 1 5 10 15
 Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys
 20 25 30
 Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp
 35 40 45
 Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala
 50 55 60
 Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly
 65 70 75 80
 Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala Glu Thr
 85 90 95
 Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly
 100 105 110
 Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Arg
 115 120 125
 Glu

<210> 31
 <211> 39
 <212> DNA
 <213> Influenza virus

<400> 31
 aggttttatc catacgacgt cccggactac gccacaact 39

<210> 32
 <211> 13
 <212> PRT
 <213> Influenza virus

<400> 32
 Arg Phe Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Thr Thr
 1 5 10

<210> 33
 <211> 384
 <212> DNA

STERN29.002APC SEQLIST.TXT

<213> Homo sapiens

<400> 33

```
ctcgagaaaa gaaatttggg gaatttccac agaatgatca agttgacgac aggaaaggaa 60
gccgcactca gttatggctt ctacggctgc cactgtggcg tgggtggcag aggatcccc 120
aaggatgcaa cggatcgctg ctgtgtcact catgactgtt gctacaaacg tctggagaaa 180
cgtggatgtg gcaccaaatt tctgagctac aagtttagca actcggggag cagaatcacc 240
tgtgcaaac aggactcctg cagaagtcaa ctgtgtgagt gtgataaggc tgctgccacc 300
tgttttgcta gaaacaagac gacctacaat aaaaagtacc agtactattc caataaacac 360
tgcagaggga gcactccacg ttgc 384
```

<210> 34

<211> 128

<212> PRT

<213> Homo sapiens

<400> 34

```
Leu Glu Lys Arg Asn Leu Val Asn Phe His Arg Met Ile Lys Leu Thr
1 5 10 15
Thr Gly Lys Glu Ala Ala Leu Ser Tyr Gly Phe Tyr Gly Cys His Cys
20 25 30
Gly Val Gly Gly Arg Gly Ser Pro Lys Asp Ala Thr Asp Arg Cys Cys
35 40 45
Val Thr His Asp Cys Cys Tyr Lys Arg Leu Glu Lys Arg Gly Cys Gly
50 55 60
Thr Lys Phe Leu Ser Tyr Lys Phe Ser Asn Ser Gly Ser Arg Ile Thr
65 70 75 80
Cys Ala Lys Gln Asp Ser Cys Arg Ser Gln Leu Cys Glu Cys Asp Lys
85 90 95
Ala Ala Ala Thr Cys Phe Ala Arg Asn Lys Thr Thr Tyr Asn Lys Lys
100 105 110
Tyr Gln Tyr Tyr Ser Asn Lys His Cys Arg Gly Ser Thr Pro Arg Cys
115 120 125
```

<210> 35

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic affinity to LPS

<400> 35

```
ccgatcatca aacttctcaa gctgcttaaa ctcttgcgcc ggaaacttct caagctgctt 60
aaactcctgc cggatcagga gtttaagcag 90
```

<210> 36

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> HA peptide containing linker

<400> 36

```
Pro Ile Ile Lys Leu Leu Lys Leu Leu Lys Leu Leu Arg Arg Lys Leu
1 5 10 15
Leu Lys Leu Leu Lys Leu Leu Pro Asp Gln Glu Phe Lys Gln
20 25 30
```

<210> 37

STERN29.002APC SEQLIST.TXT

<211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic peptide

<400> 37
 Gly Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Gly
 1 5 10 15

<210> 38
 <211> 377
 <212> PRT
 <213> Escherichia coli

<400> 38
 Met Phe Lys Thr Thr Leu Cys Ala Leu Leu Ile Thr Ala Ser Cys Ser
 1 5 10 15
 Thr Phe Ala Ala Pro Gln Gln Ile Asn Asp Ile Val His Arg Thr Ile
 20 25 30
 Thr Pro Leu Ile Glu Gln Gln Lys Ile Pro Gly Met Ala Val Ala Val
 35 40 45
 Ile Tyr Gln Gly Lys Pro Tyr Tyr Phe Thr Trp Gly Tyr Ala Asp Ile
 50 55 60
 Ala Lys Lys Gln Pro Val Thr Gln Gln Thr Leu Phe Glu Leu Gly Ser
 65 70 75 80
 Val Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg
 85 90 95
 Gly Glu Ile Lys Leu Ser Asp Pro Thr Thr Lys Tyr Trp Pro Glu Leu
 100 105 110
 Thr Ala Lys Gln Trp Asn Gly Ile Thr Leu Leu His Leu Ala Thr Tyr
 115 120 125
 Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu Val Lys Ser Ser
 130 135 140
 Ser Asp Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro Ala Trp Ala Pro
 145 150 155 160
 Gly Thr Gln Arg Leu Tyr Ala Asn Ser Ser Ile Gly Leu Phe Gly Ala
 165 170 175
 Leu Ala Val Lys Pro Ser Gly Leu Ser Phe Glu Gln Ala Met Gln Thr
 180 185 190
 Arg Val Phe Gln Pro Leu Lys Leu Asn His Thr Trp Ile Asn Val Pro
 195 200 205
 Pro Ala Glu Glu Lys Asn Tyr Ala Trp Gly Tyr Arg Glu Gly Lys Ala
 210 215 220
 Val His Val Ser Pro Gly Ala Leu Asp Ala Glu Ala Tyr Gly Val Lys
 225 230 235 240
 Ser Thr Ile Glu Asp Met Ala Arg Trp Val Gln Ser Asn Leu Lys Pro
 245 250 255
 Leu Asp Ile Asn Glu Lys Thr Leu Gln Gln Gly Ile Gln Leu Ala Gln
 260 265 270
 Ser Arg Tyr Trp Gln Thr Gly Asp Met Tyr Gln Gly Leu Gly Trp Glu
 275 280 285
 Met Leu Asp Trp Pro Val Asn Pro Asp Ser Ile Ile Asn Gly Ser Asp
 290 295 300
 Asn Lys Ile Ala Leu Ala Ala Arg Pro Val Lys Ala Ile Thr Pro Pro
 305 310 315 320
 Thr Pro Ala Val Arg Ala Ser Trp Val His Lys Thr Gly Ala Thr Gly
 325 330 335
 Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys Glu Leu Gly Ile
 340 345 350
 Val Met Leu Ala Asn Lys Asn Tyr Pro Asn Pro Ala Arg Val Asp Ala

STERN29.002APC SEQLIST.TXT

355
Ala Trp Gln Ile Leu Asn Ala Leu Gln
370 375

360
365

<210> 39
<211> 1140
<212> DNA
<213> Escherichia coli

<400> 39
atgttcaaaa cgacgctctg cgccttatta attaccgcct cttgctccac atttgctgcc 60
cctcaacaaa tcaacgatat tgtgcatcgc acaattaccc cgcttataga gcaacaaaag 120
atcccgggta tggcgggtggc ggtaatttat cagggtaaac cttattactt tacctggggc 180
tatgCGGaca tcgCCAAAAA gcagcccgtc acacagcaaa cgttgtttga gttaggttcg 240
gtcagcaaaa catttactgg cgtgcttggt ggcgacgcta ttgctcgagg ggaaatcaag 300
ttaagcgatc ccacaacaaa atactggcct gaacttaccg ctaaacagtg gaatgggatc 360
acactattac atctcgcaac ctacactgct ggcggcctgc cattgcaggt gccggatgag 420
gtgaaatcct caagcgactt gctgcgcttc tatcaaaact ggcagcctgc atgggctcca 480
ggaaacacaac gtctgtatgc caactccagt atcggtttgt tcggcgcaact ggctgtgaag 540
ccgtctgggt tgagttttga gcaggcgatg caaactcgtg tcttccagcc actcaaactc 600
aaccatacgt ggattaatgt accgcccgcga gaagaaaaga attacgcctg gggatatcgc 660
gaaggtaagg cagtgcattg ttcgcctggg gcgttagatg ctgaagctta tgggtgtgaag 720
tcgaccattg aagatatggc ccgctgggtg caaagcaatt taaaaccctt tagtactgat 780
atcaatgaga aaacgcttca acaagggata caactggcac aatctcgcta ctggcaaac 840
ggcgatatgt atcagggcct ggcgtgggaa atgctggact ggccggtaaa tcttgacagc 900
atcattaacg gcagtacaa taaaattgca ctggcagcac gccccgtaaa agcgattacg 960
cccccaactc ctgcagtacg cgcattcatg gtacataaaa caggggcgac cggcgatttt 1020
ggtagctatg tcgcgtttat tccagaaaaa gagctgggta tcgtgatgct ggcaacaaaa 1080
aactatccca atccagcgag agtcgacgcc gcctggcaga ttcttaacgc tctacagtaa 1140

<210> 40
<211> 256
<212> PRT
<213> Bacillus licheniformis

<400> 40
Met Gln Lys Glu Thr Arg Phe Leu Pro Gly Thr Asn Val Glu Tyr Glu
1 5 10 15
Asp Tyr Ser Thr Phe Phe Asp Lys Phe Ser Ala Ser Gly Gly Phe Val
20 25 30
Leu Phe Asn Ser Asn Arg Lys Lys Tyr Thr Ile Tyr Asn Arg Lys Glu
35 40 45
Ser Thr Ser Arg Phe Ala Pro Ala Ser Thr Tyr Lys Val Phe Ser Ala
50 55 60
Leu Leu Ala Leu Glu Ser Gly Ile Ile Thr Lys Asn Asp Ser His Met
65 70 75 80
Thr Trp Asp Gly Thr Gln Tyr Pro Tyr Lys Glu Trp Asn Gln Asp Gln
85 90 95
Asp Leu Phe Ser Ala Met Ser Ser Ser Thr Thr Trp Tyr Phe Gln Lys
100 105 110
Leu Asp Arg Gln Ile Gly Glu Asp His Leu Arg His Tyr Leu Lys Ser
115 120 125
Ile His Tyr Gly Asn Glu Asp Phe Ser Val Pro Ala Asp Tyr Trp Leu
130 135 140
Asp Gly Ser Leu Gln Ile Ser Pro Leu Glu Gln Val Asn Ile Leu Lys
145 150 155 160
Lys Phe Tyr Asp Asn Glu Phe Asp Phe Lys Gln Ser Asn Ile Glu Thr
165 170 175
Val Lys Asp Ser Ile Arg Leu Glu Glu Ser Asn Gly Arg Val Leu Ser
180 185 190
Gly Lys Thr Gly Thr Ser Val Ile Asn Gly Glu Leu His Ala Gly Trp

		195					200					205				
Phe	Ile	Gly	Tyr	Val	Glu	Thr	Ala	Asp	Asn	Thr	Phe	Phe	Phe	Ala	Val	
	210					215					220					
His	Ile	Gln	Gly	Glu	Lys	Arg	Ala	Ala	Gly	Ser	Ser	Ala	Ala	Glu	Ile	
225					230					235					240	
Ala	Leu	Ser	Ile	Leu	Asp	Lys	Lys	Gly	Ile	Tyr	Pro	Ser	Val	Ser	Arg	
				245					250					255		

<400>	41						
atgcaaaaag	aaacacgctt	tttaccgggc	accaatgtag	aatacgaaga	ttacagcact	60	
tttttttgata	aatttttcagc	ctcagggggc	tttgtctgt	ttaattctaa	taggaaaaag	120	
tatacaatat	acaatatggaa	agaagcacc	ttcagattcg	cacctgtctc	cacctacaag	180	
gtgttttagcg	cattgtctgc	actggaatcc	gggcatcatca	cgaagaacga	ctctcacatg	240	
acttggggatg	ggactcaata	tccgtataaa	gaatggaatc	aagaccagga	tttattctct	300	
gcgatgagca	gctccacaac	atggttatfff	caaaaattgg	accggcfaat	tggggaggat	360	
cattttacgtc	attatctcaa	atctatacat	tatggaaatg	aggatttttc	agtcctggcc	420	
gattattggc	tggatggctc	tcttcaaatt	tctccacttg	aacaggttcaa	tatatataaa	480	
aagttttatg	ataacgaatt	tgatttttaa	cagtctaata	ttgaaactgt	gaaagattcg	540	
atacgttttag	aagaatcaaa	tggcaggggt	ttatccggta	aaaccggaac	ctcggtaatc	600	
aacgggggaac	tccatgccgg	tigggtttatc	gggtatgtag	aaactgccga	taatactttt	660	
ttctttgtct	ttcataattca	aggtagaaaa	cgggtgtccg	gaagctccgc	tgccgaaatt	720	
gcactttcca	ttttagataa	aaaggggatt	tatccctccg	tttcccca		768	

<400> 42
Ala Arg Ala Leu Ala Thr Ser Leu Gln Ala Phe Ala
1 5 10

<400> 43
Ser Glu Lys Arg Glu Leu Leu Ile Asp Trp Met Lys
1 5 10

STERN29.002APC SEQLIST.TXT

<400> 44
Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
1 5 10

<210> 45
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> TEM-1 beta-lactamase alpha helix 9

<400> 45
Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu
1 5 10

<210> 46
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AmpC alpha helix 8

<400> 46
Ile Glu Asp Met Ala Arg Trp Val Gln Ser Asn Leu
1 5 10

<210> 47
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> AmpC alpha helix 9

<400> 47
Lys Thr Leu Gln Gln Gly Ile Gln Leu Ala
1 5 10

<210> 48
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> restriction cassette

<400> 48
Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala
1 5 10

<210> 49
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> restriction cassette

<400> 49

ctattaactg gcgaactact tactctagct

30

<210> 50

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> restriction cassette

<400> 50

Leu Leu Thr Gly Val Pro Leu Thr Gly Thr Leu Ala
1 5 10

<210> 51

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> restriction cassette

<400> 51

ctattaactg gggtaccct aactggcact ctagct

36

<210> 52

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> restriction cassette

<400> 52

Leu Leu Thr Gly Val Pro Pro Gly Leu Gln Leu Glu Leu Lys Pro Gly
1 5 10 15
Arg Tyr Pro Leu Thr Gly Glu Leu
20

<210> 53

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> restriction cassette

<400> 53

ctattaactg gggtaccgcc cgggctgcag ctcgagctta agcccgggcg gtacccccta 60
actggcgaac ta 72

<210> 54

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> restriction cassette

STERN29.002APC SEQLIST.TXT

<400> 54
 Leu Leu Thr Gly Val Pro Pro Gly Arg Tyr Pro Leu Thr Gly Glu Leu
 1 5 10 15

<210> 55
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> restriction cassette

<400> 55
 ctattaactg gggtaccgcc cgggcggtac cccctaactg gcgaacta

48

<210> 56
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> restriction cassette

<400> 56
 Ala Leu Glu Asp Lys Leu Pro Ser Glu Lys
 1 5 10

<210> 57
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> restriction cassette

<400> 57
 gctcttgaag ataaacttcc aagtgaaaaa

30

<210> 58
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> restriction cassette

<400> 58
 Ala Leu Glu Asp Pro Gly Lys Leu Pro Ser Glu Lys
 1 5 10

<210> 59
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> restriction cassette

<400> 59

STERN29.002APC SEQLIST.TXT
gctcttgaag atcccgggaa acttccaagt gaaaaa

36

<210> 60
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> restriction cassette

<400> 60
Val Glu Asp Gly Glu Lys Ala Ala Leu Ala
1 5 10

<210> 61
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> restriction cassette

<400> 61
gtcgaggacg gcgagaaggc cgccctcgcg

30

<210> 62
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> restriction cassette

<400> 62
Val Glu Asp Gly Glu Asp Ile Lys Ala Ala Leu Ala
1 5 10

<210> 63
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> restriction cassette

<400> 63
gtcgaggacg gcgaggatat caaggccgcc ctcgcg

36

<210> 64
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> insertion site

<400> 64
Ala Leu Glu Asp Lys Leu Pro Ser Glu Lys
1 5 10

STERN29.002APC SEQLIST.TXT

<210> 65
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> insertion site

<400> 65
 gctcttgaag ataaacttcc aagtgaaaaa

30

<210> 66
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> insertion site

<400> 66
 Ala Leu Glu Asp Pro Arg Phe Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1 5 10 15
 Thr Thr Gly Lys Leu Pro Ser Glu Lys
 20 25

<210> 67
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> insertion site

<400> 67
 gctcttgaag atcccaggtt ttatccatac gacgtcccgg actacgccac aactgggaaa 60
 cttccaagtg aaaaa 75

<210> 68
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 68
 Asn Leu Val Asn Phe His Arg Met Ile Lys Leu Thr Thr Gly Lys Glu
 1 5 10 15
 Ala Ala Leu Ser Tyr Gly Phe Tyr Gly Cys His Cys Gly Val Gly Gly
 20 25 30
 Arg Gly Ser Pro Lys Asp Ala Thr Asp Arg Cys Cys Val Thr His Asp
 35 40 45
 Cys Cys Tyr Lys Arg Leu Glu Lys Arg Gly Cys Gly Thr Lys Phe Leu
 50 55 60
 Ser Tyr Lys Phe Ser Asn Ser Gly Ser Arg Ile Thr Cys Ala Lys Gln
 65 70 75 80
 Asp Ser Cys Arg Ser Gln Leu Cys Glu Cys Asp Lys Ala Ala Ala Thr
 85 90 95
 Cys Phe Ala Arg Asn Lys Thr Thr Tyr Asn Lys Lys Tyr Gln Tyr Tyr
 100 105 110
 Ser Asn Lys
 115